

MARINE MAMMAL & TURTLE DIVISION (MMTD), PUBLICATIONS

Personnel from the Marine Mammal & Turtle Division are in “bold”

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Week of 16 September 2013

Foote, A.D., **Morin, P.A., Pitman, R.L.**, Ávila-Arcos, M.C., **Durban, J.W.**, van Helden, A., Sinding, M.-H.S., Gilbert, M.T.P., 2013. Mitogenomic insights into a recently described and rarely observed killer whale morphotype. *Polar Biology* 36, 1519-1523.

Abstract - Identifying evolutionary divergent taxonomic units, e.g. species and subspecies, is important for conservation and evolutionary biology. The ‘type D’ killer whale, *Orcinus orca*, is a rarely observed morphotype with a pelagic, circumpolar subantarctic distribution, making dedicated research and therefore taxonomic study extremely difficult to date. In this study, we used DNA target enrichment hybridisation capture coupled to high throughput sequencing, to obtain the first DNA sequence from the only known museum specimen of this recently described morphotype. The high coverage, complete mitogenome sequence was compared to a previously published global dataset of 139 individuals, indicating that this type is highly divergent to all previously genetically sequenced killer whale forms. The estimated divergence time (390,000 years ago) from its most recent common ancestor with other extant killer whale lineages was the second oldest split within the killer whale phylogeny. This study provides the first genetic support of type D potentially being a distinct subspecies or species of killer whale, although further samples are needed to identify whether there is monophyly of mitogenome sequences and whether nuclear DNA also indicates reproductive isolation. These findings also highlight the value of natural history museum collections and new technologies to investigate the taxonomy of rare, cryptic or difficult to access species.

Week of 9 September 2013

Barlow, J., P. L. Tyack, M. P. Johnson, R. W. Baird, G. S. Schorr, R. D. Andrews, and N. Aguilar de Soto. 2013. Trackline and point detection probabilities for acoustic surveys of Cuvier's and Blainville's beaked whales. *J. Acoust. Soc. Am.* 134(3): 2486-2496.

Abstract - Acoustic survey methods can be used to estimate density and abundance using sounds produced by cetaceans and detected using hydrophones if the probability of detection can be estimated. For passive acoustic surveys, probability of detection at zero horizontal distance from a sensor, commonly called $g(0)$, depends on the temporal patterns of vocalizations. Methods to estimate $g(0)$ are developed based on the assumption that a beaked whale will be detected if it is producing regular echolocation clicks directly under or above a hydrophone. Data from acoustic recording tags placed on two species of beaked whales (Cuvier's beaked whale—*Ziphius cavirostris* and Blainville's beaked whale—*Mesoplodon densirostris*) are used to directly estimate the percentage of time they produce echolocation clicks. A model of vocal behavior for these species as a function of their diving behavior is applied to other types of dive data (from time-depth recorders and time-depth-transmitting satellite tags) to indirectly determine $g(0)$ in other locations for low ambient noise conditions. Estimates of $g(0)$ for a single instant in time are 0.28 (s.d. = 0.05) for Cuvier's beaked whale and 0.19 (s.d. = 0.01) for Blainville's beaked whale.

Tina M. Yack, Jay Barlow, John Calambokidis, Brandon Southall, and Shannon Coates. 2013. Identification of previously unknown beaked whale habitat in the Southern California Bight using a towed hydrophone array. *The Journal of the Acoustical Society of America* 134(3): 2589–2595 [doi.org/10.1121/1.4816585]

Abstract - Beaked whales are diverse and species rich taxa. They spend the vast majority of their time submerged, regularly diving to depths of hundreds to thousands of meters, typically occur in small groups, and behave inconspicuously at the surface. These factors make them extremely difficult to detect using standard visual survey methods. However, recent advancements in acoustic detection capabilities have made passive acoustic monitoring (PAM) a viable alternative. Beaked whales can be discriminated from other odontocetes by the unique characteristics of their echolocation clicks. In 2009 and 2010, PAM methods using towed hydrophone arrays were tested. These methods proved highly effective for real-time detection of beaked whales in the Southern California Bight (SCB) and were subsequently implemented in 2011 to successfully detect and track beaked whales during the ongoing Southern California Behavioral Response Study. The three year field effort has resulted in (1) the successful classification and tracking of Cuvier's (*Ziphius cavirostris*), Baird's (*Berardius bairdii*), and unidentified Mesoplodon beaked whale species and (2) the identification of areas of previously unknown beaked whale habitat use. Identification of habitat use areas will contribute to a better understanding of the complex relationship between beaked whale distribution, occurrence, and preferred habitat characteristics on a relatively small spatial scale. These findings will also provide information that can be used to promote more effective management and conservation of beaked whales in the SCB, a heavily used Naval operation and training region.

Week of 2 September 2013

Edwards EF, Kellar NM, and Perrin WF. 2013. Form, function and pathology in the pantropical spotted dolphin (*Stenella attenuata*). NOAA Technical Memorandum NOAA-TMNMFS-SWFSC-516. 76pp.

Summary - This report reviews, integrates and summarizes published literature regarding form, function and pathology in the pantropical spotted dolphin. Because the pantropical spotted dolphin is one of the primary species targeted by the tuna purse-seine fishery in the eastern tropical Pacific Ocean (ETP), the report includes discussion of spotted dolphin morphological and physiological characteristics that may be negatively affected by interaction with the ETP purse-seine fishery.

Week of 12 August 2013

Okuyama J, Nakajima K, Noda T, Kimura S, Kamihata H, et al. 2013. Ethogram of Immature Green Turtles: Behavioral Strategies for Somatic Growth in Large Marine Herbivores. PLoS ONE 8(6): e65783. doi:10.1371/journal.pone.0065783.

Abstract - Animals are assumed to obtain/conserves energy effectively to maximise their fitness, which manifests itself in a variety of behavioral strategies. For marine animals, however, these behavioral strategies are generally unknown due to the lack of high-resolution monitoring techniques in marine habitats. As large marine herbivores, immature green turtles do not need to allocate energy to reproduction but are at risk of shark predation, although it is a rare occurrence. They are therefore assumed to select/use feeding and resting sites that maximise their fitness in terms of somatic growth, while avoiding predation. We investigated fine-scale behavioral patterns (feeding, resting and other behaviors), microhabitat use and time spent on each behavior for eight immature green turtles using data loggers including: depth, global positioning system, head acceleration, speed and video sensors. Immature green turtles at Iriomote Island, Japan, spent an average of 4.8 h feeding on seagrass each day, with two peaks, between 5:00 and 9:00, and between 17:00 and 20:00. This feeding pattern appeared to be restricted by gut capacity, and thus maximised energy acquisition. Meanwhile, most of the remaining time was spent resting at locations close to feeding grounds, which allowed turtles to conserve energy spent travelling and reduced the duration of periods exposed to predation. These behavioral patterns and time allocations allow immature green turtles to effectively obtain/conserves energy for growth, thus maximising their fitness.

Trego ML, Kellar NM, Danil K. 2013. Validation of Blubber Progesterone Concentrations for Pregnancy Determination in Three Dolphin Species and a Porpoise. PLoS ONE 8(7): e69709. doi:10.1371/journal.pone.0069709

Abstract - Recent studies have validated the use of biopsies as a minimally invasive way to identify pregnant females in several species of wild cetaceans: *Balaenaptera acutorostrata*, *Delphinus delphis*, *Lissodelphis borealis*, and *Lagenorhynchus obliquidens*. These studies found that progesterone (P4) concentrations quantified from blubber attached to biopsy samples is diagnostic of pregnancy. Here we examine a broader group of cetacean species in efforts to investigate how progesterone levels vary between species with respect to pregnancy status. We compared P4 concentrations in blubber collected from fishery bycatch and beach-stranded specimens for 40 females of known reproductive condition from *Delphinus capensis* (n = 18), *Stenella attenuata* (n = 8), *S. longirostris* (n = 6), and *Phocoenoides dalli* (n = 8). The P4 concentrations were different ($t = -7.1$, $p = 1.79E-08$) between pregnant and nonpregnant animals in all species, with the mean blubber P4 concentration for pregnant animals 164 times higher than that of non-pregnant animals. There was no overlap in concentration levels between sexually immature or nonpregnant sexually mature animals and pregnant animals. No significant differences ($F = 0.354$, $p = 0.559$) were found between mature non-pregnant and immature *D. capensis* and *P. dalli*, suggesting P4 level is not indicative of maturity state in female delphinoids. P4 concentrations in relation to reproductive state were remarkably similar across species. All samples were analyzed with two different enzyme immunoassay kits to gauge assay sensitivity to measure progesterone in small samples, such as biopsies. With the technique now validated for these cetacean species, blubber P4 is a reliable diagnostic of pregnancies across multiple species, and thus expands the utility of this method to study reproduction in free-ranging cetaceans using biopsies.

Week of 5 August 2013

T.J. Guy, S.L. Jennings, R.M. Suryan, E.F. Melvin, M.A. Bellman, **L.T. Ballance**, B.A. Blackie, D.A. Croll, T. Deguchi, T.O. Geernaert, R.W. Henry, M. Hester, K.D. Hyrenbach, J. Jahncke, M.A. Kappes, K. Ozaki, J. Roletto, F. Sato, W.J. Sydeman, J.E. Zamon. 2013. Overlap of North Pacific albatrosses with the U.S. west coast groundfish and shrimp fisheries. Fisheries Research 147:222-234.

Abstract - We used a combination of seabird data (both fishery-dependent and fishery-independent) and fishing-effort data to evaluate the relative fisheries risk of five west coast groundfish fisheries and one shrimp fishery to black-footed (*Phoebastria nigripes*), short-tailed (*P. albatrus*) and Laysan albatrosses (*P. immutabilis*). To assess risk, an overlap index was derived as the product of total fishing effort and at-sea survey density of black-footed albatross. This index was used as the primary tool to estimate overlap with the endangered, relatively rare short-tailed albatross, which show similar habitat utilization from satellite telemetry tracks. Telemetry data indicate Laysan albatross primarily occur offshore beyond observed fishing effort. Black-footed and short-tailed albatross-fishery overlap was highest at the shelf-break (201–1000 m) north of 36°N. Overlap and reported albatross mortality indicate that the sablefish (*Anoplopoma fimbria*) longline and Pacific hake (*Merluccius productus*) catcher-processor fisheries pose the greatest risk to these species; the near-shore rockfish (*Sebastes* spp.) longline, pink shrimp (*Pandalus jordani*) trawl, California halibut (*Paralichthys californicus*) trawl, and non-hake groundfish trawl fisheries pose relatively little risk. Implementing proven seabird bycatch-reduction measures will likely minimize albatross mortality in the highest-risk fishery, sablefish longline.

Week of 29 July 2013

Edward D. Weber and **Thomas J. Moore**. Published Online. Corrected conversion algorithms for the CalCOFI station grid and their implementation in several computer languages. CalCOFI Reports.

Abstract - Converting between geographic coordinates in latitude and longitude and the line and station sampling pattern of the California Cooperative Fisheries Investigations (CalCOFI) program is a commonly

required task for conducting research on the California Current ecosystem. This note presents several corrections and clarifications to the previously published algorithms for performing these conversions. We include computer code to implement the algorithms in Java™, Perl, Python, and R. We note that freely available code to conduct the conversions in Fortran, Matlab®, JavaScript™, and Visual Basic® has previously been published, and an online conversion tool is also available. A future version of the PROJ.4 cartographic projections library will also include support for CalCOFI conversions, thereby allowing for convenient conversions using the GRASS GIS, PostGIS, Python, Perl, R, and many other programs and programming languages.

Week of 15 July 2013

J. E. Van Noord, E. A. Lewallen and **R. L. Pitman**. 2013. Flyingfish feeding ecology in the eastern Pacific: prey partitioning within a speciose epipelagic community. *Journal of Fish Biology*. doi:10.1111/jfb.12173

Abstract – To test the hypothesis that prey partitioning contributes to community stability in flyingfish, the gut contents of 359 flyingfish specimens (representing five genera and eight species within Exocoetidae and Hemiramphidae) were collected at 50 dip-net stations during hour-long night-time fishing in oceanic waters of the eastern tropical Pacific Ocean between August and November 2007. Analyses using multidimensional scaling, and analysis of similarity revealed significant dietary differences among species, and similarity percentages tests helped identify the specific prey taxa responsible for these differences. Six species specialized on copepods ($58 \cdot 3$ – $96 \cdot 9\%$ by number), but targeted different families. Specifically, the barbel flyingfish *Exocoetus monocirrhus* ($n = 205$) focused on euchaetids ($51 \cdot 6\%$), the banded flyingfish *Hirundichthys marginatus* ($n = 24$) fed on pontellids ($21 \cdot 8\%$), while the tropical two-wing flyingfish *Exocoetus volitans* ($n = 11$) and the bigwing halfbeak *Oxyporhamphus micropterus* ($n = 34$) ingested calanoids ($54 \cdot 6$ and $17 \cdot 0\%$). In contrast, the whitetip flyingfish *Cheilopogon xenopterus* ($n = 73$) and the mirrorwing flyingfish *Hirundichthys speculiger* ($n = 4$) had generalized diets comprising similar proportions of amphipod, copepod, mollusc and larval fish prey. Distinct differences in mean fullness, highly digested material, per cent empty guts and mean numbers of prey per gut were also synthesized, and uncovered a pattern of asynchronous feeding. Altogether, these findings provide valuable descriptive data on the diets of an understudied group of epipelagic teleosts, and, by extension, suggest that prey partitioning (taxa and feeding times) may influence flyingfish feeding ecology by reducing interspecific competition.

Kim M. Parsons, **John W. Durban**, Alexander M. Burdin, Vladimir N. Burkanov, **Robert L. Pitman**, Jay Barlow, Lance G. Barrett-Lennard, Richard G. LeDuc, **Kelly M. Robertson**, Craig O. Matkin, and Paul R. Wade. 2013. Geographic Patterns of Genetic Differentiation among Killer Whales in the Northern North Pacific. *Journal of Heredity*. doi:10.1093/jhered/est037

Abstract - The difficulties associated with detecting population boundaries have long constrained the conservation and management of highly mobile, wide-ranging marine species, such as killer whales (*Orcinus orca*). In this study, we use data from 26 nuclear microsatellite loci and mitochondrial DNA sequences (988 bp) to test a priori hypotheses about population subdivisions generated from a decade of killer whale surveys across the northern North Pacific. A total of 462 remote skin biopsies were collected from wild killer whales primarily between 2001 and 2010 from the northern Gulf of Alaska to the Sea of Okhotsk, representing both the piscivorous “resident” and the mammal-eating “transient” (or Bigg’s) killer whales. Divergence of the 2 ecotypes was supported by both mtDNA and microsatellites. Geographic patterns of genetic differentiation were supported by significant regions of genetic discontinuity, providing evidence of population structuring within both ecotypes and corroborating direct observations of restricted movements of individual whales. In the Aleutian Islands (Alaska), subpopulations, or groups with significantly different mtDNA and microsatellite allele frequencies, were largely delimited by major oceanographic boundaries for resident killer whales. Although Amchitka Pass represented a major subdivision for transient killer whales between the central and western Aleutian Islands, several smaller subpopulations were evident throughout the eastern

Aleutians and Bering Sea. Support for seasonally sympatric transient subpopulations around Unimak Island suggests isolating mechanisms other than geographic distance within this highly mobile top predator.

Carretta, J. V., S. M. Wilkin, M. M. Muto, and K. Wilkinson. 2013. Sources of human-related injury and mortality for U.S. Pacific west coast marine mammal stock assessments, 2007-2011. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-514, 83 p.

Abstract – The Marine Mammal Protection Act (MMPA) requires the National Oceanic and Atmospheric Administration (NOAA), National Marine Fisheries Service (NMFS), to document human-caused mortality, non-serious injury (NSI), and serious injury (SI) of marine mammals as part of assessing marine mammal stocks and to evaluate human-caused injury and mortality levels in the context of potential biological removal (PBR) levels calculated under the MMPA (Wade 1998). NMFS defines SI as “any injury that will likely result in mortality.” While recognizing mortality is straightforward, distinguishing NSI from SI requires reliable data on injury severity and animal condition, often in challenging environments where thorough examination of injuries is not possible. NMFS updated its SI designation and reporting process, which uses guidance from previous SI workshops (Angliss and DeMaster 1998, Andersen *et al.* 2008), expert opinion, and analysis of historic injury cases to develop new criteria for distinguishing SI from NSI (NOAA 2012, Moore *et al.* 2013).

This report contains records of human-caused injury and mortality to pinnipeds and cetaceans from 2007 to 2011, for marine mammal populations that occur in U.S. west coast waters and which are evaluated in Pacific region marine mammal stock assessment reports (SARs) (Carretta *et al.* 2013). Mortality records, while included, were obviously not evaluated for SI/NSI status. Subsistence and directed takes are not reported here but are reported in SARs published by NMFS.

Sources of injury data include strandings, disentanglement networks, and fishery observer programs. Stranding network data includes records of injured marine mammals at sea and ashore reported by the public, as well as researchers working in these same areas. Injury sources include, but are not limited to, *vessel strikes, gillnet entanglement, pot and trap gear entanglement, shootings, marine debris entanglement, research-related injuries/deaths, hook and line fishery interactions, and power plant water intake entrainment*. This report covers the 5-year period of 2007 to 2011, which includes injury and mortality data used in preparation of draft 2013 Pacific marine mammal stock assessments. Most records originate from stranding networks in California, Oregon, and Washington, though a few Alaska records of Eastern North Pacific gray whales (*Eschrichtius robustus*) are included, because this population is assessed in the Pacific region SARs and occurs along the U.S. west coast. Other marine mammals such as Steller sea lions (*Eumetopias jubatus*) occur in California, Oregon, and Washington waters, but they are assessed in Alaska region SARs and not included in this report (Allen and Angliss 2013). Injury determinations for Pacific region species/stocks in the central Pacific from Hawaii westward are also included in separate reports.

Week of 8 July 2013

Shannon Rankin, Jay Barlow, Yvonne Barkley, and Robert Valtierra. 2013. A guide to constructing hydrophone arrays for passive acoustic data collection during NMFS shipboard cetacean surveys. NOAA Technical Memorandum, NOAA-TM-NMFS-SWFSC-511.

Overview - This report provides a step-by-step guide to constructing a modular oil-filled towed hydrophone array to be used for passive acoustic monitoring of cetaceans from ships. This report was based on a workshop hosted by SWFSC to teach acousticians from the other NMFS science centers how to construct this hardware (funding provided by NOAA’s Advanced Sampling Technologies Working Group).

Jefferson, T.A., C.R. Weir, R.C. Anderson, **L.T. Ballance**, R.D. Kenney, and J.J. Kiszka. 2013. Global patterns of Risso’s dolphin (*Grampus griseus*) distribution: a review and critical evaluation. Mammal Review. doi:10.1111/mam.12008

Abstract - 1. The global range of Risso's dolphin *Grampus griseus* is not well known, and there has been confusion in the literature as to whether the species has a broad, circumglobal range or only occurs along continental margins.

2. To clarify the species' distribution and habitat preferences, we compiled and reviewed all available (published and unpublished) records of sightings and captures of this species for the past 62 years (1950–2012, n = 8068 records). Stranding records were not included.

3. The results showed that the species has a range that extends across ocean basins and spans between at least 64°N and 46°S, and is apparently absent from high latitude polar waters. Although Risso's dolphins occur in all habitats from coastal to oceanic, they show a strong range-wide preference for mid-temperate waters of the continental shelf and slope between 30° and 45° latitude.

4. Although a number of misconceptions about the distributional ecology of Risso's dolphin have existed, this analysis showed that it is a widespread species. It strongly favours temperate waters and prefers continental shelf and slope waters to oceanic depths. These habitat preferences appear to hold throughout much or all of the species' range.

Week of 1 July 2013

Davison, P. C., D. M. Checkley Jr., J. A. Koslow, and **J. Barlow**. 2013. Carbon export mediated by mesopelagic fishes in the northeast Pacific Ocean. *Progress in Oceanography*

Abstract - The role of fishes in the global carbon cycle is poorly known and often neglected. We show that the biomass of mesopelagic fishes off the continental USA west to longitude 141°W is positively related to annual net primary productivity, and averages 17 g m⁻². We estimate the export of carbon out of the epipelagic ocean mediated by mesopelagic fishes ("fish-mediated export"; FME) with individual-based metabolic modeling using the catch from 77 mesopelagic trawls distributed over the study area. FME was 15–17% (22–24 mg C m⁻² d⁻¹) of the total carbon exported in the study area (144 mg C m⁻² d⁻¹), as estimated from satellite data. FME varies spatially in both magnitude and relative importance. Although the magnitude of FME increases with increasing total export, the ratio of FME to total export decreases. FME exceeds 40% of the total carbon export in the oligotrophic North Pacific Subtropical Gyre, but forms <10% of the total export in the most productive waters of the California Current. Because the daytime residence depth of these fishes is below the depths where most remineralization of sinking particles occurs, FME is approximately equal to the passive transport at a depth of 400 m. The active transport of carbon by mesopelagic fishes and zooplankton is similar in magnitude to the gap between estimates of carbon export obtained with sediment traps and by other methods. FME should be considered in models of the global carbon cycle.

Week of 24 June 2013

Andrew D. Foote, **Phillip A. Morin**, **Robert L. Pitman**, Mari'a C. A'vila-Arcos, **John W. Durban**, Anton van Helden, Mikkel-Holger S. Sinding, M. Thomas P. Gilbert. 2013. Mitogenomic insights into a recently described and rarely observed killer whale morphotype. *Polar Biology* DOI 10.1007/s00300-013-1354-0

Abstract - Identifying evolutionary divergent taxonomic units, e.g. species and subspecies, is important for conservation and evolutionary biology. The 'type D' killer whale, *Orcinus orca*, is a rarely observed morphotype with a pelagic, circumpolar subantarctic distribution, making dedicated research and therefore taxonomic study extremely difficult to date. In this study, we used DNA target enrichment hybridisation capture coupled to high throughput sequencing, to obtain the first DNA sequence from the only known museum specimen of this recently described morphotype. The high coverage, complete mitogenome sequence was compared to a previously published global dataset of 139 individuals, indicating that this type is highly divergent to all previously genetically sequenced killer whale forms. The estimated divergence time (390,000 years ago) from its most recent common ancestor with other extant killer whale lineages was the second oldest split within the killer whale phylogeny. This study provides the first genetic support of type D

potentially being a distinct subspecies or species of killer whale, although further samples are needed to identify whether there is monophyly of mitogenome sequences and whether nuclear DNA also indicates reproductive isolation. These findings also highlight the value of natural history museum collections and new technologies to investigate the taxonomy of rare, cryptic or difficult to access species.

Van Noord, J. E., R. J. Olson, **J. V. Redfern**, and R. S. Kaufmann. 2013. Diet and prey selectivity in three surface-migrating myctophids in the eastern tropical Pacific. *Ichthyological Research*:1-4.

<http://link.springer.com/article/10.1007/s10228-013-0350-2>

Abstract - To test feeding selectivity, the diets of three surface-migrating myctophids [*Myctophum nitidulum* ($n = 299$), *Symbolophorus reversus* ($n = 199$), and *Gonichthys tenuiculus* ($n = 82$)] were compared to zooplankton prey collections at 32 stations in the eastern Pacific Ocean, August–November 2006. *Myctophum nitidulum* fed predominately on copepods (42.7 % by number) and ostracods (41.5 %), selected amphipods ($p = 0.002$) and ostracods ($p = 0.014$), and avoided copepods ($p < 0.001$). *Symbolophorus reversus* fed on copepods (32.5 % by number) and euphausiids (29.6 %) and selected euphausiids ($p = 0.002$) and amphipods ($p = 0.008$). *Gonichthys tenuiculus* fed on ostracods (34.6 %) and amphipods (27.3 %), but showed no significant selectivity.

Week of 17 June 2013

Paul C. Fiedler, Jessica V. Redfern, Joel Van Noord, Candice Hall, Robert L. Pitman, Lisa T. Ballance. 2013. Effects of a tropical cyclone on a pelagic ecosystem from the physical environment to top predators. *Marine Ecology Progress Series* 484:1-16.

Abstract - Tropical cyclones are environmental disturbances that may have important effects on open-ocean ecosystem structure and function, but their overall impact has rarely been assessed. The Stenella Abundance Research Line Transect and Ecosystem (STARLITE) survey, in August–November 2007, investigated spatial and temporal ecosystem variability in the eastern tropical Pacific Ocean off southwestern Mexico. Oceanographic, plankton, flyingfish, seabird, and cetacean sampling was conducted along eight 170 km transect lines, each of which were surveyed on 2 consecutive days at ~3 wk intervals. Tropical storm Kiko passed through the study area on 15–17 October and forced changes in the physical environment and in the ecosystem, from plankton to top predators. Kiko mixed water from beneath the strong, shallow thermocline to the surface. As a result, surface temperature decreased by 0.6°C, the thermocline and chlorophyll maximum layer shoaled by 10–20 m, stratification decreased by 27%, and chlorophyll increased by 33% at the surface and 35% over the euphotic zone. These changes persisted for at least 4 wk. Zooplankton biomass increased by 59% about 3 wk after the phyto-plankton increase. Changes in the stomach fullness and diet composition of planktivorous flyingfish were consistent with the increase in zooplankton biomass. Among top predators, the sighting rate of dolphins declined, while the response of seabirds varied by species and was confounded by seasonal migration patterns. Tropical cyclones are a recurrent disturbance in this region. They initiate a bottom-up forcing of the ecosystem, creating persistent patches of higher primary and secondary production, and may be regarded as a disturbance regime.

Available at <http://www.int-res.com/articles/feature/m484p001.pdf>

Week of 10 June 2013

Simone Baumann-Pickering, **Tina M. Yack, Jay Barlow**, Sean M. Wiggins and John A. Hildebrand. 2013. Baird's beaked whale echolocation signals. *J. Acoust. Soc. Am.* 133 (6).

Abstract - Echolocation signals from Baird's beaked whales were recorded during visual and acoustic shipboard surveys of cetaceans in the California Current ecosystem and with autonomous, long-term recorders in the Southern California Bight. The preliminary measurement of the visually validated Baird's

beaked whale echolocation signals from towed array data were used as a basis for identifying Baird's signals in the autonomous recorder data. Two distinct signal types were found, one being a beaked whale-like frequency modulated (FM) pulse, the other being a dolphin-like broadband click. The median FM inter-pulse interval was 230 ms. Both signal types showed a consistent multi-peak structure in their spectra with peaks at 9, 16, 25, and 40 kHz. Depending on signal type, as well as recording aspect and distance to the hydrophone, these peaks varied in relative amplitude. The description of Baird's echolocation signals will allow for studies of their distribution and abundance using towed array data without associated visual sightings and from autonomous seafloor hydrophones.

Fritz L, Sweeney K, Johnson D, **Lynn M**, Gelatt T, and **Gilpatrick J**. 2013. Aerial and ship-based surveys of Steller Sea Lions (*Eumetopias jubatus*) conducted in Alaska in June-July 2008 through 2012, and an update on the status and trend of the western Distinct Population Segment in Alaska. NOAA Tech. Memo. NMFS-AFSC-251

Abstract - There is strong evidence that both the western and eastern distinct population segments (DPSs) of Steller sea lion (*Eumetopias jubatus*) increased in overall abundance in Alaska between 2000 and 2012. Counts of both non-pups (adults and juveniles) and pups during the breeding season in the western DPS were lowest in 2000, and increased at average rates of 1.67% per year (95% credible interval of 1.01-2.38% per year) and 1.45% per year (0.69-2.22% per year), respectively through 2012. However, there was considerable regional variability in non-pup and pup trends in 2000-2012 across the western DPS, with strong evidence of increases in three of the four regions east of Samalga Pass (eastern and western Gulf of Alaska, and eastern Aleutian Islands; ranges of 2.39% per year to 4.51% per year for non-pups and 3.03% per year to 3.97% per year for pups) being offset somewhat by both weak and strong declines in the two regions west of Samalga Pass (central and western Aleutian Islands; slow, uncertain declines in the central [-0.56% per year and -0.46% per year for non-pups and pups, respectively] and steep, certain declines in the western Aleutians [-7.23% per year and -9.36% per year for non-pups and pups, respectively]). Within the central Aleutian Islands, non-pup and pup trends varied east and west of 177°W (roughly Tanaga Pass): in the two rookery cluster areas to the east, trends were generally positive (0.51% per year and 2.25% per year for non-pups, and 2.56% per year and 0.45% per year for pups), while to the west, there was strong evidence of decline (-4.48% per year and -3.24% per year for non-pups, and -4.83% per year and -1.74% per year for pups). In southeast Alaska (eastern DPS of Steller sea lion), both non-pup and pup counts increased between 2000 and 2010, continuing the upward trend begun in the mid-1970s.

Movement of young Steller sea lions into and out of the eastern Gulf of Alaska was observed during surveys conducted 'early' and 'late' in 2008, 2009 and 2010. Analysis of the movement of sea lions branded as pups in 2000-2011 on rookeries extending from southeast Alaska through the Kodiak archipelago (including work by Jemison et al. in review) suggests a net movement from the central to the eastern Gulf of Alaska of ~1,600 sea lions during the breeding season, as well as a smaller net movement (of ~180 sea lions) from southeast Alaska to the western DPS. Inter-regional movement of this magnitude within the western DPS could affect regional trend estimation, and therefore it may be inappropriate to treat the eastern and central Gulf of Alaska as 'closed' populations; non-pup counts in the combined eastern-central Gulf of Alaska increased at 2.40% per year between 2000 and 2012. Average annual inter-DPS movement represents < 0.5% of the total number of sea lions counted in the western DPS and < 1% of those counted in southeast Alaska, and likely had a negligible impact on overall trend estimates in either area.

If the overall western non-pup count in Alaska continues to increase through 2015, the western DPS appears to be on a trajectory to satisfy the first demographic criterion for down-listing from 'endangered' to 'threatened' status under the Endangered Species Act (NMFS 2008). The second demographic criterion, however, involves regional population performance, which has varied across the range. The western DPS may satisfy the first part of criterion #2 if non-pup counts in the eastern, central and western Gulf of Alaska, eastern Aleutian Islands, and Russia (overall) continue to increase through 2015. However, persistent declines in the western Aleutian Islands and the western half of the central Aleutian Islands may preclude it from satisfying the second part of criterion #2, and indicate that the western DPS is responding to meso-scale variability in factors affecting recovery.

Roden SE, Morin PA, Frey A, Balazs GH, Zarate P, Cheng I-J, Dutton PH. 2013.

Green turtle population structure in the Pacific: new insights from SNPs and microsatellites. *Endangered Species Research* 20: 227–234, doi: 10.3354/esr00500

Abstract: A set of nuclear single nucleotide polymorphisms (SNPs) and microsatellite markers was used to detect genetic stock structure among 5 Pacific green turtle *Chelonia mydas* nesting populations. We sampled populations in the Galapagos Islands, Ecuador (n = 57), Colola, Mexico (n = 75), French Frigate Shoals, Hawaii (n = 141), Yap, Micronesia (n = 73), and Wan-an, Taiwan (n = 57), to represent eastern, central, and western Pacific regions. A combination of 29 single independent SNPs and linked SNPs combined as haplotypes were used for a total of 20 independent markers. In addition, 8 polymorphic microsatellite markers were applied to the same sample set. Both sets of nuclear markers confirmed significant differentiation between all sampled populations in the 3 Pacific regions ($p \leq 0.001$). The use of these SNPs and microsatellites resulted in sufficient power to detect small population differences not seen in previous studies using smaller numbers of nuclear markers. Our results suggest that male-mediated gene flow between regional nesting stocks is more limited than previously believed, allowing the potential to delineate stocks more clearly. Finally, we discuss the value of SNP markers as an alternative or complement to other nuclear markers such as microsatellites for the examination of stock structure.

Week of 20 May 2013

Archer FI, Morin PA, Hancock-Hanser BL, Robertson KM, Leslie MS, et al. 2013. Mitogenomic Phylogenetics of Fin Whales (*Balaenoptera physalus* spp.): Genetic Evidence for Revision of Subspecies. *PLoS ONE* 8(5): e63396. doi:10.1371/journal.pone.0063396

Abstract - There are three described subspecies of fin whales (*Balaenoptera physalus*): *B. p. physalus* Linnaeus, 1758 in the Northern Hemisphere, *B. p. quoyi* Fischer, 1829 in the Southern Hemisphere, and a recently described pygmy form, *B. p. patachonica* Burmeister, 1865. The discrete distribution in the North Pacific and North Atlantic raises the question of whether a single Northern Hemisphere subspecies is valid. We assess phylogenetic patterns using ~16 K base pairs of the complete mitogenome for 154 fin whales from the North Pacific, North Atlantic - including the Mediterranean Sea - and Southern Hemisphere. A Bayesian tree of the resulting 136 haplotypes revealed several well-supported clades representing each ocean basin, with no haplotypes shared among ocean basins. The North Atlantic haplotypes (n = 12) form a sister clade to those from the Southern Hemisphere (n = 42). The estimated time to most recent common ancestor (TMRCA) for this Atlantic/Southern Hemisphere clade and 81 of the 97 samples from the North Pacific was approximately 2 Ma. 14 of the remaining North Pacific samples formed a well-supported clade within the Southern Hemisphere. The TMRCA for this node suggests that at least one female from the Southern Hemisphere immigrated to the North Pacific approximately 0.37 Ma. These results provide strong evidence that North Pacific and North Atlantic fin whales should not be considered the same subspecies, and suggest the need for revision of the global taxonomy of the species.

Katarina Topalov, Arndt Schimmelmann, P. David Polly, Peter E. Sauer, and **Mark Lowry.** 2013. Environmental, trophic, and ecological factors influencing bone collagen $\delta^2\text{H}$. *Geochimica et Cosmochimica Acta* 111:88-104.

Summary Organic deuterium/hydrogen stable isotope ratios (i.e. $^2\text{H}/^1\text{H}$, expressed as $\delta^2\text{H}$ value in ‰) in animal tissues are related to the $^2\text{H}/^1\text{H}$ in diet and ingested water. Bone collagen preserves the biochemical $^2\text{H}/^1\text{H}$ isotopic signal in the $\delta^2\text{H}$ value of collagen's non-exchangeable hydrogen. Therefore, $\delta^2\text{H}$ preserved in bone collagen has the potential to constrain environmental and trophic conditions, which is of interest to researchers studying of both living and fossil vertebrates. Our data examine the relationship of $\delta^2\text{H}$ values of collagen with geographic variation in $\delta^2\text{H}$ of meteoric waters, with local variations in the ecology and trophic level of species, and with the transition from mother's milk to adult diet. Based on 97 individuals from 22 marine and terrestrial vertebrates (predominately mammals), we found the relationships of collagen $\delta^2\text{H}$ to both geographic variation in meteoric water $\delta^2\text{H}$ ($R^2=0.55$) and to $\delta^{15}\text{N}$ in bone collagen ($R^2=0.17$)

statistically significant but weaker than previously reported. The second strongest control on collagen $\delta^2\text{H}$ in our data is dietary, with nearly fifty percent of the variance in $\delta^2\text{H}$ explained by trophic level ($R^2=0.47$). Trophic level effects potentially confound the local meteoric signal if not held constant: herbivores tend to have the lowest $\delta^2\text{H}$ values, omnivores have intermediate ones, and carnivores have the highest values. Body size (most likely related to mass-specific metabolic rates) has a strong influence on collagen $\delta^2\text{H}$ ($R^2=0.30$), by causing greater sensitivity in smaller animals to seasonal climate variations and/or high evapotranspiration leading to ^2H -enrichment in tissues. In marine mammals weaning produces a dramatic effect on collagen $\delta^2\text{H}$ with adult values being universally higher than pup values ($R^2=0.79$). Interestingly, the shift in $\delta^{15}\text{N}$ at weaning is downward, even though normally hydrogen and nitrogen isotope ratios are positively correlated with one another in respect to trophic level. Our findings suggest that in carnivores, which have an especially high variance in $\delta^2\text{H}$, large samples are needed to separate signals from precipitation, trophic level, body size, and age. For $\delta^2\text{H}$ of fossil collagen to be useful as a proxy of environmental or dietary information, these confounding effects need to be understood, which means careful selection of a study species. Further, $\delta^2\text{H}$ from a single fossil bone collagen is likely to be uninterpretable.

Week of 13 May 2013

Moore JE, Curtis KA, Lewison RL, Dillingham PW, Cope JM, Fordham SV, Heppell SS, Pardo SA, Simpfendorfer CA, Tuck GN, Zhou S. 2013. Evaluating sustainability of fisheries bycatch mortality for marine megafauna: a review of conservation reference points for data-limited populations. *Environmental Conservation* (online First View), doi:10.1017/S037689291300012X

Summary - Fisheries bycatch threatens populations of marine megafauna such as marine mammals, turtles, seabirds, sharks and rays, but fisheries impacts on non-target populations are often difficult to assess due to factors such as data limitation, poorly defined management objectives and lack of quantitative bycatch reduction targets. Limit reference points can be used to address these issues and thereby facilitate adoption and implementation of mitigation efforts. Reference points based on catch data and life history analysis can identify sustainability limits for bycatch with respect to defined population goals even when data are quite limited. This can expedite assessments for large numbers of species and enable prioritization of management actions based on mitigation urgency and efficacy. This paper reviews limit reference point estimators for marine megafauna bycatch, with the aim of highlighting their utility in fisheries management and promoting best practices for use. Different estimators share a common basic structure that can be flexibly applied to different contexts depending on species life history and available data types. Information on demographic vital rates and abundance is required; of these, abundance is the most data-dependent and thus most limiting factor for application. There are different approaches for handling management risk stemming from uncertainty in reference point and bycatch estimates. Risk tolerance can be incorporated explicitly into the reference point estimator itself, or probability distributions may be used to describe uncertainties in bycatch and reference point estimates, and risk tolerance may guide how those are factored into the management process. Either approach requires simulation-based performance testing such as management strategy evaluation to ensure that management objectives can be achieved. Factoring potential sources of bias into such evaluations is critical. This paper reviews the technical, operational, and political challenges to widespread application of reference points for management of marine megafauna bycatch, while emphasizing the importance of developing assessment frameworks that can facilitate sustainable fishing practices.

TRACEY J. REGAN, BARBARA L. TAYLOR, GRANT G. THOMPSON, JEAN FITTS COCHRANE, KATHERINE RALLS, MICHAEL C. RUNGE, AND RICHARD MERRICK. 2013. Testing Decision Rules for Categorizing Species' Extinction Risk to Help Develop Quantitative Listing Criteria for the U.S. Endangered Species Act. *Conservation Biology* DOI: 10.1111/cobi.12055

Abstract - Lack of guidance for interpreting the definitions of endangered and threatened in the U.S. Endangered Species Act (ESA) has resulted in case-by-case decision making leaving the process vulnerable to being considered arbitrary or capricious. Adopting quantitative decision rules would remedy this but

requires the agency to specify the relative urgency concerning extinction events over time, cutoff risk values corresponding to different levels of protection, and the importance given to different types of listing errors. We tested the performance of 3 sets of decision rules that use alternative functions for weighting the relative urgency of future extinction events: a threshold rule set, which uses a decision rule of x% probability of extinction over y years; a concave rule set, where the relative importance of future extinction events declines exponentially over time; and a shoulder rule set that uses a sigmoid shape function, where relative importance declines slowly at first and then more rapidly. We obtained decision cutoffs by interviewing several biologists and then emulated the listing process with simulations that covered a range of extinction risks typical of ESA listing decisions. We evaluated performance of the decision rules under different data quantities and qualities on the basis of the relative importance of misclassification errors. Although there was little difference between the performance of alternative decision rules for correct listings, the distribution of misclassifications differed depending on the function used. Misclassifications for the threshold and concave listing criteria resulted in more overprotection errors, particularly as uncertainty increased, whereas errors for the shoulder listing criteria were more symmetrical. We developed and tested the framework for quantitative decision rules for listing species under the U.S. ESA. If policy values can be agreed on, use of this framework would improve the implementation of the ESA by increasing transparency and consistency.

Robertson, K. M., Minich, J., Bowman, A. J. and P. A. Morin. 2013. A thin soup: Extraction and amplification of DNA from DMSO and ethanol used as preservative for cetacean tissue samples. Conservation Genet Resour DOI 10.1007/s12686-013-9934-4.

Summary - Two popular tissue preservatives, 100% ethanol and 20% salt saturated dimethyl sulfoxide (DMSO) solution were tested for the existence of amplifiable, free-floating DNA after 2 to 18 yrs of tissue storage. We found that short mtDNA fragments were consistently amplified and sequenced from DMSO preservative, while nDNA amplification was limited and inconsistent. Amplification of both mtDNA and nDNA failed most of the time for the ethanol samples.

Week of 6 May 2013

BARBARA GALLETTI VERNAZZANI, ELSA CABRERA, and **ROBERT L. BROWNELL, JR.** 2013. Eastern south Pacific southern right whale photo-identification catalog reveals behavior and habitat use patterns. Marine Mammal Science doi:10.1111/mms.12030
(No Abstract)

Jepson PD, Deaville R, et al., incl **R. L. Brownell, Jr.** (2013) What Caused the UK's Largest Common Dolphin (*Delphinus delphis*) Mass Stranding Event? PLoS ONE 8(4): e60953. doi:10.1371/journal.pone.0060953

Abstract - On 9 June 2008, the UK's largest mass stranding event (MSE) of short-beaked common dolphins (*Delphinus delphis*) occurred in Falmouth Bay, Cornwall. At least 26 dolphins died, and a similar number was refloated/herded back to sea. On necropsy, all dolphins were in good nutritive status with empty stomachs and no evidence of known infectious disease or acute physical injury. Auditory tissues were grossly normal (26/26) but had microscopic haemorrhages (5/5) and mild otitis media (1/5) in the freshest cases. Five lactating adult dolphins, one immature male, and one immature female tested were free of harmful algal toxins and had low chemical pollutant levels. Pathological evidence of mud/seawater inhalation (11/26), local tide cycle, and the relative lack of renal myoglobinuria (26/26) suggested MSE onset on a rising tide between 06:30 and 08:21 hrs (9 June). Potential causes excluded or considered highly unlikely included infectious disease, gas/fat embolism, boat strike, by-catch, predator attack, foraging unusually close to shore, chemical or algal toxin exposure, abnormal weather/climatic conditions, and high-intensity acoustic inputs from seismic airgun arrays or natural sources (e.g., earthquakes). International naval exercises did occur in close proximity to the MSE with the most intense part of the exercises (including mid-frequency sonars) occurring four days before the MSE and resuming with helicopter exercises on the morning of the MSE. The MSE may therefore have been a "two-stage process" where a group of normally pelagic dolphins entered Falmouth Bay and, after 3–4 days in/around the Bay, a second acoustic/disturbance

event occurred causing them to strand *en masse*. This spatial and temporal association with the MSE, previous associations between naval activities and cetacean MSEs, and an absence of other identifiable factors known to cause cetacean MSEs, indicates naval activity to be the most probable cause of the Falmouth Bay MSE.

Week of 30 April 2013

Jacobson, E. K., T. M. Yack, and J. Barlow. 2013. Evaluation of an automated acoustic beaked whale detection algorithm using multiple validation and assessment methods. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-509, 26 p.

Abstract - Currently, the acoustic detection of beaked whales during passive acoustic surveys requires trained acousticians to identify beaked whale signals with the aid of various software programs. The development of reliable automated detection and classification methods will enable passive acoustic approaches to better meet monitoring needs for real-time mitigation of industry and military impacts. During ongoing development of automated beaked whale detectors and classifiers it will be important for researchers at different institutions to utilize standardized metrics of performance. At the Southwest Fisheries Science Center (SWFSC), automated detection algorithms for Cuvier's beaked whale (*Ziphius cavirostris*) and Baird's beaked whale (*Berardius bairdii*) were developed using PAMGUARD software (Douglas Gillespie: www.pamguard.org). To evaluate the performance of these beaked whale detectors, 15 ten-minute recording segments were processed in PAMGUARD, and the resulting signal detections were compared to manual logs of beaked whale signals confirmed by an experienced acoustician. The comparison was conducted using three methods: precise timestamp matching between manual and automated detections, detection counts from one-minute time bins, and binary presence/absence detection classification of one-minute bins. The detections were scored as true positive, false positive, false negative or false classification. Detector efficacy was quantified using measures developed for information retrieval systems (precision, recall, and F-score) as well as the Receiver Operating Characteristic. Calculated performance scores were compared across evaluation methods. We found that the method used to evaluate detector functionality greatly influences the resulting performance scores and subsequently our perception of detector ability. Therefore, it will be important for researchers to clearly communicate methods and results of detector evaluation. To allow for greatest precision and applicability to different recording datasets, we recommend that beaked whale detectors be evaluated using timestamp matching between manual and automated detections in trial datasets and that F-scores be used to compare detectors. This approach avoids problems associated with binning datasets by eliminating the need for a measure of false negatives.

Evans, Jonathan P. and Eric M. **Keen.** 2013. Regeneration Failure in a Remnant Stand of Pignut Hickory (*Carya glabra*) on a Protected Barrier Island in Georgia, USA. *Natural Areas Journal*, 33(2):171-176.

Abstract - Maritime forest communities on barrier islands along the Atlantic and Gulf coasts have been severely fragmented by a continuous history of human land use and natural disturbance. Isolated populations of certain tree species in maritime forest fragments may now be too small to be viable and their inability to regenerate may result in their eventual elimination from barrier islands. Using an 11-year study of a population of pignut hickory (*Carya glabra*), a common species of remnant maritime forest stands on St. Catherine's Island, Georgia, we present a case study of tree regeneration failure on a barrier island. We found that there has been no recruitment of new hickory individuals into the canopy of this population over the last 65 years. Field evidence of browse and a strong correlation between seedling density distributions and microsite protection from herbivory suggest that this trend in recruitment failure is related to an increased abundance of deer (*Odocoileus*) and pigs (*Sus*) on the island. Using a size class population projection model, we estimated that, if such recruitment failure and mortality rates continue, the hickory population will be extirpated from the maritime forest within 200 years. Tree species that are failing to regenerate within maritime forests represent a special challenge that is not currently being addressed in the long-term management of barrier island biodiversity.

Week of 16 April 2013

Barlow, J. 2013. Inferring Trackline Detection Probabilities from Differences in Apparent Densities of Beaked Whales and Dwarf & Pygmy Sperm Whales in Different Survey Conditions. NOAA Technical Memorandum, NOAA-TM-508.

Abstract - Visual line-transect surveys are commonly used to estimate the abundance of cetaceans (whales, dolphins, and porpoises). A key parameter in this method is the probability of detecting a cetacean that is directly on the transect line or $g(0)$. Beaked whales and dwarf & pygmy sperm whales are visually inconspicuous and dive for long periods of time. Previous studies have shown that trackline detection probability is low for these species even in the best survey conditions. Trackline detection probability has never been estimated for them in poor survey conditions. A method is developed here to estimate the relative values of trackline detection probability by comparing estimates of apparent density in different survey conditions (measured as Beaufort state) using estimated density in the best survey conditions as a reference point. Using data from line-transect surveys in the eastern tropical Pacific, this approach yields consistent estimates of trackline detection probability for beaked whales and for dwarf & pygmy sperm whales as functions of sighting conditions in two adjacent study areas. Results show that $g(0)$ for beaked whales is similar for Beaufort 0 and 1 conditions but decreases with increasing Beaufort to less than 10% of that value in Beaufort 5. For dwarf & pygmy sperm whales $g(0)$ decreases even faster with Beaufort state and, in Beaufort 2, is less than 10% of its value in Beaufort 0. These relative values of $g(0)$ are used to extrapolate published estimates of $g(0)$ for calm seas to yield values for Beaufort states 0 to 5.

Week of 8 April 2013

C. S. Baker, A. Hutt, K. Thompson, M. L. Dalebout, J. Robins, **R. L. Brownell Jr.** & G. S. Stone. 2013. Species identity and human consumption of beaked whales in the Gilbert Islands, Republic of Kiribati. Animal Conservation doi:10.1111/acv.12039

Abstract - We investigated the species identity and local use of cetaceans on the Gilbert Islands, Republic of Kiribati. Working with the Kiribati Ministry of Environment, Lands and Agricultural Development and Fisheries Division, we visited the islands of Tarawa, Tabiteuea (North), Butaritari and Onotoa from June to July 2009, and collected 24 bones, bone fragments or teeth attributed to recent strandings. The mitochondrial DNA control region or cytochrome *b* was successfully amplified from 12 bones or bone fragments and used to identify four species: *Mesoplodon* sp. representing a new species or subspecies of beaked whale, the dense-beaked whale *Mesoplodon densirostris*, Cuvier's beaked whale *Ziphius cavirostris* and the pygmy sperm whale *Kogia breviceps*. This is the first confirmed identification of the dense-beaked, Cuvier's and pygmy sperm whales from the Gilbert Islands. All specimens were reportedly used for human consumption.

Jone TT, **Seminoff JA**. 2013. Feeding Biology: Advances from Field-Based Observations, Physiological Studies, and Molecular Techniques. In: Musick, J., J. Wyneken, and K. Lohman (Eds.), Biology of the Sea Turtles, Volume 3. CRC Press, Boca Raton, FL. pp. 211-248.

Summary - Since Archie Carr's seminal work in the 1960s and 1970s and efforts by Karen Bjorndal and others in the 1980s and 1990s, feeding biology has been a relatively well-studied facet of sea turtle biology. This is opportune for the science of sea turtles considering that nutrient acquisition strategies are among the most important components of a sea turtle's life history, influencing key demographic parameters such as somatic growth, age-at-maturity, and timing of reproductive migrations. Over the past two decades, however, the advent of new research fields such as physiological monitoring, biologging, and stable isotope analysis (SIA) have helped strengthen this understanding even further. These tools have provided insights that have in some cases confirmed earlier wisdom about how a sea turtle makes a living, and in other cases have redefined long-standing biological paradigms. Considering the new information that has come available, it is clear that the ecological strategies of some species are much more diverse than originally considered. For

example, green turtles (*Chelonia mydas*), long-considered obligate neritic herbivores instead eat large amounts of animal matter in many places, and at least in the Pacific are commonly high-seas dwellers, even as adults. Hawksbill turtles (*Eretmochelys imbricata*), the “coral reef dwelling” turtle, are turning up in the strangest of places. In the eastern Pacific, for example, adult hawksbills inhabit mangrove estuaries during non-breeding periods, a huge departure from our belief that the species was tied to coral reefs. In the Caribbean and Indian Ocean, hawksbills are now known to depend on seagrass pastures for foraging and residence. Leatherbacks (*Dermochelys coriacea*), historically defined as “high-seas inhabitants,” are now seen in coastal habitats more than ever before. These and other novel revelations about feeding biology are at least partly due to the globalization of sea turtle research and an everexpanding toolbox at the disposal of field and laboratory scientists. Indeed, more research with both traditional and novel tools is conducted in more parts of the world than ever before, and we are now gaining an appreciation of just how complex and adaptive sea turtles can be. Much new biological information has emerged in the published literature since *The Biology of the Sea Turtles* (Volume 1) was first published and a thorough update is warranted, particularly for aspects relating to feeding biology. In this chapter we present new information for all seven sea turtle species, building on Karen Bjørndal’s chapter on Feeding Biology in Volume 1 that summarized what was known at that time. In Section 9.2 we present the latest information about sea turtle diet and feeding biology. Here we describe new diet items and novel foraging tactics that are reshaping our perceptions about the types of prey consumed and methods by which sea turtles access food resources. In Section 9.3 we focus on the feeding physiology of sea turtles (e.g., specific dynamic action (SDA), digestive efficiency, and passage rates of digesta), a still-understudied area of sea turtle feeding biology, but one that is expanding thanks to additional field and lab-based scientific research. Understanding how sea turtle energy acquisition is constrained by physiological and environmental factors is important as these data factor into growth rates, residency times, population demographics, bioenergetics and energy budgets, and reproductive output. In Sections 9.4 (stable isotopes) and 9.5 (fatty acids and trace elements) we explore the “molecular-based” techniques that are showing great promise for establishing diet, trophic status, and foraging movements of sea turtles. Clearly, the advent of these approaches allows us to learn much about the types of foods consumed by turtles based on the analysis of their own body tissues. As described earlier, the feeding biology of sea turtles is a broad topic with many nuances. Together the established (e.g., stomach content analysis, esophageal lavage) and emerging (e.g., SIA, fatty acids) techniques give greater insight and understanding into the unique foraging strategies of sea turtles both intra- and interspecifically and through life-history stages. Studies of feeding physiology then begin to tie together what, when, and where sea turtles eat with why and how they eat to meet daily and yearly energy demands of maintenance, growth, and reproduction. In the end, our goal is to provide an update on the current knowledge of sea turtle feeding biology and share a perspective of how our understanding has evolved in the past decades.

MacDonald BD, Madrak SV, Lewison RL, **Seminoff JA, Eguchi T.** 2013. Fine scale diel movement of the east Pacific green turtle, *Chelonia mydas*, in a highly urbanized foraging environment. *Journal of Experimental Marine Biology and Ecology* 443:56–64.

Abstract - Protection of endangered species requires an understanding of their spatial ecology in relation to human activities. Recent improvements in monitoring technologies, such as automated acoustic telemetry, have enabled the collection of these data for mobile marine organisms such as sea turtles. The east Pacific green sea turtle *Chelonia mydas* uses San Diego Bay, CA, a heavily developed ecosystem, as a year-round foraging ground. We used a combination of manual and automated acoustic telemetry from 2009 to 2011 to elucidate the distribution of green turtles throughout South San Diego Bay and to understand their diel behavior. Tracked turtles ($n = 20$) ranged in size from 54.9 to 102.5 cm straight carapace length and had fidelity to two sites: the warm-water effluent channel of a waterfront power plant and an eelgrass meadow. Turtles tracked manually during the night were more sedentary (mean swimming speed \pm SE: 0.38 ± 0.03 km h⁻¹) and generally restricted their activity to waters near the power plant. During the day, turtles swam at higher speeds (0.67 ± 0.07 km h⁻¹) and were mainly found in eelgrass meadows where they are known to forage. Turtles were occasionally found near a shipping terminal, which occurred almost exclusively during the daytime. Turtles in areas of increased boat traffic are at risk of vessel strikes, and future monitoring should investigate the potential for turtle–human interactions in other heavily-used areas of San Diego Bay.

Future monitoring should also characterize how turtle behavior may change following the decommissioning of the power plant, which occurred six months before the end of this study.

Week of 1 April 2013

Becker EA, KA Forney, MC Ferguson, J Barlow, JV Redfern. 2012. Predictive Modeling of Cetacean Densities in the California Current Ecosystem based on Summer/Fall Ship Surveys in 1991- 2008. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-499, 45 p.

Abstract - We use data from six ship-based cetacean and ecosystem assessment surveys in the California Current Ecosystem (CCE) to update habitat-based density models for 11 species and one small-beaked-whale guild. We previously had modeled cetacean density as a function of oceanic variables for the same 12 species/guild using data collected during four line-transect ship surveys conducted in the CCE in summer and fall of 1991, 1993, 1996, and 2001. An independent set of survey data collected in the summer and fall of 2005 was used to validate the models. These estimates were incorporated into a web-based system that allows users to estimate cetacean density within any user-defined region within the CCE study area. In this study, data from an additional line-transect survey conducted in 2008 were pooled with the 1991-2005 data and used to re-build the habitat-based density models. We also refit the 1991-2008 data to the previous “best” models to compare model performance. The additional year of data provided increased sample sizes and a greater range of oceanic conditions for robust model development. Predicted densities for each year were smoothed and then averaged to produce a composite grid that represents our best estimate of CCE cetacean density over the past 20 years. The final model predictions were used to update the web-based system and also provided to the U.S. Navy to help assess potential impacts from their at-sea training and testing activities.

Carretta, J.V., E. Oleson, D.W. Weller, A.R. Lang, K.A. Forney, J. Baker, B. Hanson, K. Martien, M.M. Muto, M.S. Lowry, J. Barlow, D. Lynch, L. Carswell, R. L. Brownell Jr., D. K. Mattila, and M.C. Hill. 2013. U.S. Pacific Marine Mammal Stock Assessments: 2012. U.S. Department of Commerce, NOAA Technical Memorandum, NMFS-SWFSC-504. 378 p.

Available at <http://swfsc.noaa.gov/prd-sars/>

Frey A, Dutton PH, and Balazs GH (2013) Insights on the demography of cryptic nesting by green turtles (*Chelonia mydas*) in the main Hawaiian Islands from genetic relatedness analysis. *Journal of Experimental Marine Biology and Ecology* 442: 80–87 <http://dx.doi.org/10.1016/j.jembe.2013.01.030>

Abstract - Within the Hawaiian archipelago, green turtle nesting has occurred almost exclusively in the northwestern Hawaiian Islands, mainly at French Frigate Shoals (FFS), however an increase in occasional nesting has recently been observed on the main Hawaiian Islands (MHI). Due to logistical constraints, monitoring the nesting activity on the MHI has been limited to nest documentation. Without systematic tagging of the nesting females it is not clear how many are nesting here. We used mitochondrial (mt) DNA sequencing combined with nuclear (n) DNA analysis based on 14 microsatellite markers to infer the number of individual nesters. Genotypes were determined for 181 dead embryos and hatchlings salvaged from 71 nests laid on Maui, Molokai, Kauai, Lanai, and Oahu, along with those of 81 nesting females that were sampled on FFS. MtDNA results showed that 58% of the MHI clutches were laid by females with a relatively rare haplotype only reported in 16% of the FFS nesting population. Nuclear DNA results showed that nesting in the MHI might be attributed to a relatively small number of females that appear to be related to each other. We were able to reconstruct genotypes for nesting females from hatchling profiles and we estimate that 15 different females were responsible for clutches laid on the MHI. Taken together, the mtDNA and nDNA results suggest that the nesting population at the MHI may be the result of a few founders that originated from the FFS breeding population, possibly facilitated by captive rearing and release of FFS juveniles locally from Oahu. We suggest that this regional range expansion may buffer against the loss of current nesting sites at FFS due to sea level rise. Our results demonstrate the potential for genetic tools to be

incorporated into population assessment, particularly in areas where access to reproductive females is difficult and population size is unknown.

Ruiz-Cooley, R.I., L.T. Ballance, and M.D. McCarthy. 2013. Range expansion of the jumbo squid in the NE Pacific: $\delta^{15}\text{N}$ decrypts multiple origins, migration and habitat use. PLoS ONE 8(3):e59651. doi:10.1371/journal/pone.0059651.

Abstract - Coincident with climate shifts and anthropogenic perturbations, the highly voracious jumbo squid *Dosidicus gigas* reached unprecedented northern latitudes along the NE Pacific margin post 1997–98. The physical or biological drivers of this expansion, as well as its ecological consequences remain unknown. Here, novel analysis from both bulk tissues and individual amino acids (Phenylalanine; Phe and Glutamic acid; Glu) in both gladii and muscle of *D. gigas* captured in the Northern California Current System (NCCS) documents for the first time multiple geographic origins and migration. Phe $\delta^{15}\text{N}$ values, a proxy for habitat baseline $\delta^{15}\text{N}$ values, confirm at least three different geographic origins that were initially detected by highly variable bulk $\delta^{15}\text{N}$ values in gladii for squid at small sizes (<30 cm gladii length). In contrast, bulk $\delta^{15}\text{N}$ values from gladii of large squid (>60 cm) converged, indicating feeding in a common ecosystem. The strong latitudinal gradient in Phe $\delta^{15}\text{N}$ values from composite muscle samples further confirmed residency at a point in time for large squid in the NCCS. These results contrast with previous ideas, and indicate that small squid are highly migratory, move into the NCCS from two or more distinct geographic origins, and use this ecosystem mainly for feeding. These results represent the first direct information on the origins, immigration and habitat use of this key “invasive” predator in the NCCS, with wide implications for understanding both the mechanisms of periodic *D. gigas* population range expansions, and effects on ecosystem trophic structure.

Weller, D.W., Bettridge, S., **Brownell, R.L., Jr.,** Laake, J.L., **Moore, J.E.,** Rosel, P.E., **Taylor, B.L** and Wade, P.R. 2013. Report of the National Marine Fisheries Service gray whale stock identification workshop. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-507

Summary - A single population stock of gray whales (*Eschrichtius robustus*), referred to as the eastern North Pacific (ENP) stock, is presently recognized in U.S. waters. New information, however, suggests the possibility of recognizing two additional stocks of gray whales in U.S. waters: the Pacific Coast Feeding Group (PCFG) and the western North Pacific (WNP) stock. To evaluate the currently recognized and potentially emerging characterization of gray whale stock structure, NMFS established a scientific Task Force (TF). The overarching objective of this TF was to provide an objective scientific evaluation of gray whale stock structure as defined under the MMPA and implemented through the NMFS Guidelines for Assessing Marine Mammal Stocks (GAMMS; NMFS 2005). More specifically, the TF was convened to provide advice on the primary question – “*Is the PCFG a “population stock” under the MMPA and GAMMS guidelines?*” In addition, the TF was asked to provide advice on a question of developing importance – “*Is the WNP stock a “population stock” under the MMPA and GAMMS guidelines?*”

Week of 25 March 2013

Redfern, J. V., M. F. McKenna, T. J. Moore, J. Calambokidis, M. L. DeAngelis, E. A. Becker, J. Barlow, K. A. Forney, P. C. Fiedler, and S. J. Chivers. 2013. Assessing the risk of ships striking large whales in marine spatial planning. Conservation Biology 27:292-302.

Abstract - Marine spatial planning provides a comprehensive framework for managing multiple uses of the marine environment and has the potential to minimize environmental impacts and reduce conflicts among users. Spatially explicit assessments of the risks to key marine species from human activities are a requirement of marine spatial planning. We assessed the risk of ships striking humpback (*Megaptera novaeangliae*), blue (*Balaenoptera musculus*), and fin (*Balaenoptera physalus*) whales in alternative shipping routes derived from patterns of shipping traffic off Southern California (U.S.A.). Specifically, we developed whale-habitat models and assumed ship-strike risk for the alternative shipping routes was proportional to the

number of whales predicted by the models to occur within each route. This definition of risk assumes all ships travel within a single route. We also calculated risk assuming ships travel via multiple routes. We estimated the potential for conflict between shipping and other uses (military training and fishing) due to overlap with the routes. We also estimated the overlap between shipping routes and protected areas. The route with the lowest risk for humpback whales had the highest risk for fin whales and vice versa. Risk to both species may be ameliorated by creating a new route south of the northern Channel Islands and spreading traffic between this new route and the existing route in the Santa Barbara Channel. Creating a longer route may reduce the overlap between shipping and other uses by concentrating shipping traffic. Blue whales are distributed more evenly across our study area than humpback and fin whales; thus, risk could not be ameliorated by concentrating shipping traffic in any of the routes we considered. Reducing ship-strike risk for blue whales may be necessary because our estimate of the potential number of strikes suggests that they are likely to exceed allowable levels of anthropogenic impacts established under U.S. laws.

Tiwari, M. 2012. Sea Turtle surveys in the Southern Nicobar Islands: Results of surveys from February-May 1991. Indian Ocean Turtle Newsletter 16: 14-18. NO ABSTRACT

Week of 11 March 2013

Stewart KR, James MC, Roden S and Dutton PH. 2013. Assignment tests, telemetry, and tag-recapture data converge to identify natal origins of leatherback turtles, *Dermochelys coriacea*, foraging in Canadian waters. Journal of Animal Ecology DOI: 10.1111/1365-2656.12056.
<http://onlinelibrary.wiley.com/journal/10.1111/%28ISSN%291365-2656/earlyview>

Summary

1. Investigating migratory connectivity between breeding and foraging areas is critical to effective management and conservation of highly mobile marine taxa, particularly threatened, endangered, or economically important species that cross through regional, national and international boundaries.
2. The leatherback turtle (*Dermochelys coriacea*, Vandelli 1761) is one such transboundary species that spends time at breeding areas at low latitudes in the northwest Atlantic during spring and summer. From there, they migrate widely throughout the North Atlantic, but many show fidelity to one region off eastern Canada, where critical foraging habitat has been proposed. Our goal was to identify nesting beach origins for turtles foraging here.
3. Using genetics, we identified natal beaches for 288 turtles that were live-captured off the coast of Nova Scotia, Canada. Turtles were sampled (skin or blood) and genotyped using 17 polymorphic microsatellite markers. Results from three assignment testing programs (ONCOR, GeneClass2 and Structure) were compared. Our nesting population reference data set included 1417 individuals from nine Atlantic nesting assemblages. A supplementary data set for 83 foraging turtles traced to nesting beaches using flipper tags and/or PIT tags (n = 72), or inferred from satellite telemetry (n = 11), enabled ground-truthing of the assignments.
4. We first assigned turtles using only genetic information and then used the supplementary recapture information to verify assignments. ONCOR performed best, assigning 64 of the 83 recaptured turtles to natal beaches (77.1%). Turtles assigned to Trinidad (164), French Guiana (72), Costa Rica (44), St. Croix (7), and Florida (1) reflect the relative size of those nesting populations, although none of the turtles were assigned to four other potential source nesting assemblages.
5. Our results demonstrate the utility of genetic approaches for determining source populations of foraging marine animals and include the first identification of natal rookeries of male leatherbacks, identified through satellite telemetry and verified with genetics. This work highlights the importance of long-term monitoring and tagging programmes in nesting and high-use foraging areas. Moreover, it provides a scientific basis for evaluating stock-specific effects of fisheries on migratory marine species, thus identifying where coordinated international recovery efforts may be most effective.

Week of 3 March 2013

Kathleen E. Hunt, Michael J. Moore, Rosalind M. Rolland, **Nicholas M. Kellar**, Ailsa J. Hall, Joanna Kershaw, Stephen A. Raverty, Cristina E. Davis, Laura C. Yeates, Teresa K. Rowles, and Scott D. Kraus. *In Review*. Opening the biggest black box: New approaches to the study of conservation physiology of large whales. Conservation Physiology.

Abstract- Large whales are subjected to a variety of conservation pressures that could be better monitored and managed if physiological information could be gathered readily from free-swimming whales. However, traditional approaches to studying physiology have been impractical for large whales, since there is no routine method for capture of the largest species and there is presently no practical method of obtaining blood samples from free-swimming whales. We review novel techniques for gathering physiological information on large whales using a variety of nonlethal and minimally invasive (or noninvasive) sample matrices. We focus on methods that should produce information relevant to conservation physiology, e.g. measures relevant to stress physiology, reproductive status, nutritional status, immune response, health, and disease. Four types of samples are discussed: fecal samples, respiratory samples ("blow"), skin/blubber samples, and photographic imaging. Fecal samples have historically been used for diet analysis but increasingly are also used for hormonal analyses, as well as for assessment of exposure to toxins, pollutants, and parasites. Blow samples contain many hormones as well as respiratory microbes, metabolites, and a variety of immune-related measures. Biopsy dart samples are widely used for genetic and contaminant analyses and are now being used for endocrine studies along with proteomic and transcriptomic approaches. Photographic analyses have benefited from recently developed quantitative techniques allowing assessment of skin condition, ectoparasite load, and nutritional status, along with wounds and scars from ship strike and fishing gear entanglement. Field application of these novel techniques has the potential to greatly improve our understanding of the physiology of large whales, better enabling assessment of the relative impacts of many anthropogenic and ecological pressures.

Week of 25 February 2013

Peter H. Dutton, Suzanne Roden, Kelly R. Stewart, Erin LaCasella, Manjula Tiwari, Angela Formia, Joao Carlos Thomé, Suzanne R. Livingstone, Scott Eckert, Didiher Chacon-Chaverri, Philippe Rivalan, Phil Allman. Population stock structure of leatherback turtles (*Dermochelys coriacea*) in the Atlantic revealed using mtDNA and microsatellite markers. Conservation Genetics DOI 10.1007/s10592-013-0456-0.

Abstract - This study presents a comprehensive genetic analysis of stock structure for leatherback turtles (*Dermochelys coriacea*), combining 17 microsatellite loci and 763 bp of the mtDNA control region. Recently discovered eastern Atlantic nesting populations of this critically endangered species were absent in a previous survey that found little ocean-wide mtDNA variation. We added rookeries in West Africa and Brazil and generated longer sequences for previously analyzed samples. A total of 1,417 individuals were sampled from 9 nesting sites in the Atlantic and SW Indian Ocean. We detected additional mtDNA variation with the longer sequences, identifying ten polymorphic sites that resolved a total of ten haplotypes, including three new variants of haplotypes previously described by shorter sequences. Population differentiation was substantial between all but two adjacent rookery pairs, and F_{ST} values ranged from 0.034 to 0.676 and 0.004 to 0.205 for mtDNA and microsatellite data respectively, suggesting that male-mediated gene flow is not as widespread as previously assumed. We detected weak ($F_{ST} = 0.008$ and 0.006) but significant differentiation with microsatellites between the two population pairs that were indistinguishable with mtDNA data. POWSIM analysis showed that our mtDNA marker had very low statistical power to detect weak structure ($F_{ST} < 0.005$), while our microsatellite marker array had high power. We conclude that the weak differentiation detected with microsatellites reflects a fine scale level of demographic independence that warrants recognition, and that all 9 of the nesting colonies should be considered as Demographically Independent Populations (DIPs) for conservation. Our findings illustrate the importance of evaluating the power of specific genetic markers to detect structure in order to correctly identify the appropriate population units to conserve.

Koch V, Peckham H, Mancini A, **Eguchi T**. 2013. Estimating At-Sea Mortality of Marine Turtles from Stranding Frequencies and Drifter Experiments. PLoS ONE 8(2): e56776. doi:10.1371/journal.pone.0056776

Abstract - Strandings of marine megafauna can provide valuable information on cause of death at sea. However, as stranding probabilities are usually very low and highly variable in space and time, interpreting the results can be challenging. We evaluated the magnitude and distribution of at-sea mortality of marine turtles along the Pacific coast of Baja California Sur, Mexico during 2010–11, using a combination of counting stranded animals and drifter experiments. A total of 594 carcasses were found during the study period, with loggerhead (62%) and green turtles (31%) being the most common species. 87% of the strandings occurred in the southern Gulf of Ulloa, a known hotspot of loggerhead distribution in the Eastern Pacific. While only 1.8% of the deaths could be definitively attributed to bycatch (net marks, hooks), seasonal variation in stranding frequencies closely corresponded to the main fishing seasons. Estimated stranding probabilities from drifter experiments varied among sites and trials (0.05–0.8), implying that only a fraction of dead sea turtles can be observed at beaches. Total mortality estimates for 15-day periods around the floater trials were highest for PSL, a beach in the southern Gulf of Ulloa, ranging between 11 sea turtles in October 2011 to 107 in August 2010. Loggerhead turtles were the most numerous, followed by green and olive ridley turtles. Our study showed that drifter trials combined with beach monitoring can provide estimates for death at sea to measure the impact of small-scale fisheries that are notoriously difficult to monitor for by-catch. We also provided recommendations to improve the precision of the mortality estimates for future studies and highlight the importance of estimating impacts of small-scale fisheries on marine megafauna.

Week of 18 February 2013

Jelsh, Jr., J. R. and **A. E. Henry**. Intra-organ flexibility in the eared grebe *Podiceps nigricollis* stomach: a spandrel in the belly. Journal of Avian Biology 44: 001–005, 2013doi: 10.1111/j.1600-048X.2012.00059.x

Abstract - Adjustments in body composition over the annual cycle have been documented in many organs and muscle groups. Here we consider the nature and significance of intra-organ variation in the eared grebe *Podiceps nigricollis* stomach, a large and variable organ that can weigh ~ 30 g when birds are staging, drop to 8–11 g before setting off, or to as little as 6.6 g after a several-day migration. Weight reduction in association with migration is conventionally regarded as an adaptation to reduce wing loading and flight costs. This interpretation applies to the premigratory reduction of the entire stomach. However, it does not fit the differential in-flight reduction of the proventriculus, because grebes require a large proventriculus to initiate digestion, and its smaller size when they need to rebuild the entire stomach and resume feeding quickly is opposite that expected in a functional context. We view the reduction of the proventriculus as a non-adaptive response, or spandrel, stemming from its intrinsically higher turnover rate. Starving birds, like migrants, also need to digest food quickly. In their case, the proventriculus is maintained as body weight declines and the gizzard is sacrificed. Mechanisms by which individual organisms achieve different responses to similar challenges, including starvation, merit further investigation.

Week of 11 February 2013

Becker, E. A., K. A. Forney, D. G. Foley, and J. Barlow. 2012. Density and spatial distribution patterns of cetaceans in the central North Pacific based on habitat models. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-490, 34 p.

Abstract - Habitat-based density models were developed for cetaceans in the Central North Pacific based on cetacean survey data collected by the Southwest Fisheries Science Center in 1997–2006. Cetacean sighting data were collected on systematic line-transect surveys in the temperate eastern Pacific, around Hawaii and other Pacific Islands, and in the eastern tropical Pacific west of 120 degrees longitude. Habitat variables, derived from satellite data, included sea surface temperature, sea surface chlorophyll, sea surface height root-

mean-square, primary productivity, distance to land, latitude, and longitude. Models were developed for the pantropical spotted dolphin, spinner dolphin, striped dolphin, rough-toothed dolphin, common bottlenose dolphin, false killer whale, short-finned pilot whale, sperm whale, Bryde's whale, and an "other dolphins" group that included the short-beaked common and Pacific white-sided dolphin. Uniform densities were estimated for species/guilds that had insufficient sightings for modeling, including pygmy killer whale, Risso's dolphin, killer whale, a small beaked whale guild (including Cuvier's beaked whale and beaked whales of the genus *Mesoplodon*), and pygmy/dwarf sperm whale. Although validation using an independent survey was not possible, modeled density estimates for the 10 species/species group were compared to previously published line-transect density estimates derived within the U.S. Exclusive Economic Zone around Hawaii. The model-based estimates of abundance fall within the 95% confidence limits of the standard line-transect analyses, and they provide greater spatial resolution of the density estimates based on habitat associations. These new models are intended as baseline density estimates for Navy planning and environmental impact statements, to be updated and improved as additional survey data become available in the future.

Moore, J., and D. Weller. 2013. Probability of taking a western gray whale during the proposed Makah hunt. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-SWFSC-507, 13 p.

Executive Summary - Recent observations of gray whales (*Eschrichtius robustus*) identified in the western North Pacific (WNP) migrating to areas off the coast of North America (Alaska to Mexico) raise concern about the possibility of the small western population being subjected to the gray whale hunt proposed by the Makah Indian Tribe in northern Washington, USA. To address this concern, we estimated the probability of striking (i.e. killing or seriously injuring) a WNP whale during the Makah hunt using six models from 4 model sets that varied based on the assumptions and types of data used for estimation. Model set 1 used WNP and ENP abundance estimates. Model set 2 used these abundance estimates, as well as sightings data from the proposed hunt area. Model sets 3 and 4 used only the sightings data. Within model sets 1 and 2, two models (A and B) differed based upon whether migrating ENP and WNP whales were assumed to be equally available to the hunt per capita (A) or whether this assumption is relaxed (B). We consider Model 2B the most plausible of all models because model set 2 makes use of all available information and 2B contains fewer assumptions than 2A. Based on model 2B, the probability of striking ≥ 1 WNP whale in a single season ranges from 0.007 to 0.036, depending on if the median or upper 95th percentile estimate is used and on which maximum is used for the total number of whales struck. The probability of striking ≥ 1 WNP whale out of 5 seasons ranges from 0.036 to 0.170 across the same scenarios. The expected number to be struck in a single year ranges from 0.01 to 0.04 and from 0.04 to 0.19 across 5 years. For context, these strike estimates were compared to different possible values of Potential Biological Removal (PBR). We also summarized analogous estimates for the number of WNP whales that would be "taken" non-lethally, in terms of the number of attempted but unsuccessful strikes as well as the number of animals approached and pursued during the hunt.

Week of 4 February 2013

Curry, BE, K.Ralls, **R.L. Brownell Jr.** 2013. Prospects for captive breeding of poorly known small cetacean species. *Endangered Species Research* 19:223-243.

Abstract - Because of the precarious condition of small cetacean species and subpopulations listed as Endangered or Critically Endangered by the IUCN, use of captive breeding for conservation has been suggested for some of them, and will likely be suggested for others. A successful captive breeding program for a new species cannot be implemented until reliable capture and husbandry techniques have been developed. Techniques for assisted reproduction and reintroduction may also be needed. We review attempts to capture, maintain, and breed poorly known small cetaceans and discuss assisted reproductive technologies (ART) that have been used to enhance captive breeding efforts for other small cetaceans. We conclude that the techniques required for successful captive breeding of most Endangered or Critically Endangered small cetacean species have not been sufficiently developed. Development of these techniques should begin before

a species or population is Critically Endangered. In particular, ARTs tend to be species specific, necessitating considerable time, money, and research to develop for each species of concern. Critically Endangered populations cannot afford to lose the individuals needed for technique development. The fairly large captive population sizes necessary (to avoid loss of genetic diversity, inbreeding, and genetic adaptation to captivity), limited space available in aquariums, and high costs of captive breeding and reintroduction programs make it unlikely that captive breeding will play a major role in the conservation of most small cetaceans. The substantive conservation measures needed to prevent extinction of Critically Endangered small cetaceans is reduction or elimination of their primary threats, which are usually by-catch and habitat loss.

Fiedler, P. C., R. Mendelssohn, D. M. Palacios, and S. J. Bograd. 2013. Pycnocline variations in the eastern tropical and North Pacific, 1958–2008. *J. Climate* 26:583–599.

Abstract - Climatic variability of the pycnocline in the eastern tropical and North Pacific has oceanographic and ecological implications. Gridded monthly profiles of temperature and salinity from the Simple Ocean Data Assimilation (SODA) reanalysis, 1958–2008, were used to derive estimates of four variables related to the density structure of the upper-ocean water column: surface temperature, pycnocline depth, mixed layer depth, and stratification (potential energy anomaly). The pycnocline is primarily a thermal gradient in this region, except in subarctic waters at the northern extreme of the study area, where salinity becomes more important than temperature in determining stratification. Spatial patterns of mean and standard deviation of the four pycnocline variables are presented. Partitioning of variance between seasonal and interannual scales shows the predominance of interannual variability in the tropics and seasonal variability at higher latitudes. Low-frequency variations (trends) in the pycnocline variables were derived by state-space analysis of time series averaged in 5° squares. Regionally coherent trends were either monotonic over 50 years or had decadal-scale changes in sign (± 5 –10-m depth, $\pm 5\%$ –10% of stratification). For example, in the eastern equatorial Pacific, the pycnocline shoaled by 10 m and weakened by 5% over the 50 years, while in the California Current the pycnocline deepened by ~5 m but showed little net change in stratification, which weakened by 5% to the mid-1970s, strengthened by 8% to the mid-1990s, and then weakened by 4% to 2008. These observed changes in the pycnocline, and future changes resulting from global climate change, may have important biological and ecosystem effects.

Hancock-Hanser, B.L., A. Frey, M.S. Leslie, P.H. Dutton, F.I. Archer, and P.A. Morin. 2013. Targeted multiplex next-generation sequencing: advances in techniques of mitochondrial and nuclear DNA sequencing for population genomics. *Molecular Ecology Resources* doi: 10.1111/1755-0998.12059

Abstract - Next-generation sequencing (NGS) is emerging as an efficient and cost-effective tool in population genomic analyses of nonmodel organisms, allowing simultaneous resequencing of many regions of multi-genomic DNA from multiplexed samples. Here, we detail our synthesis of protocols for targeted resequencing of mitochondrial and nuclear loci by generating indexed genomic libraries for multiplexing up to 100 individuals in a single sequencing pool, and then enriching the pooled library using custom DNA capture arrays. Our use of DNA sequence from one species to capture and enrich the sequencing libraries of another species (i.e. cross-species DNA capture) indicates that efficient enrichment occurs when sequences are up to about 12% divergent, allowing us to take advantage of genomic information in one species to sequence orthologous regions in related species. In addition to a complete mitochondrial genome on each array, we have included between 43 and 118 nuclear loci for low-coverage sequencing of between 18 kb and 87 kb of DNA sequence per individual for single nucleotide polymorphisms discovery from 50 to 100 individuals in a single sequencing lane. Using this method, we have generated a total of over 500 whole mitochondrial genomes from seven cetacean species and green sea turtles. The greater variation detected in mitogenomes relative to short mtDNA sequences is helping to resolve genetic structure ranging from geographic to species-level differences. These NGS and analysis techniques have allowed for simultaneous population genomic studies of mtDNA and nDNA with greater genomic coverage and phylogeographic resolution than has previously been possible in marine mammals and turtles.

Pitman, R. L. 2013. Clipperton Island. Pp. 471-473, in Robert Warren Howarth (ed.), *Biomes and Ecosystems: An Encyclopedia*. Salem Press, Ipswich, MA.

Week of 22 January 2013

X. Zhao, D. Wang, S. T. Turvey, **B. Taylor** and T. Akamatsu. Distribution patterns of Yangtze finless porpoises in the Yangtze River: implications for reserve management. *Animal Conservation* doi:10.1111/acv.12019

Abstract - The Yangtze finless porpoise (*Neophocaena asiaeorientalis asiaeorientalis*) is a highly threatened cetacean endemic to the middle and lower reaches of the Yangtze River that has suffered a dramatic decline in recent decades. We characterize and quantify recent distribution patterns of porpoises in the Yangtze River in order to facilitate strategic management of existing *in situ* cetacean reserves and maximize effective utilization of limited conservation resources. We calculated porpoise relative abundance (encounter rate) using a 1-km moving average along the Yangtze main stem based on a combined visual and acoustic survey conducted in 2006. We then evaluated conservation priority areas based on encounter rates along the river. High-porpoise density areas (> 0.20 porpoises km⁻¹) cover approximately one-third (33.9%, 599 km) of the survey area and contain approximately two-thirds of the porpoise population, making them priority areas for porpoise conservation. In contrast, low-porpoise density areas (0.05 porpoises km⁻¹) cover 28.8% (509 km) of the survey area but contain only 4.5% of the porpoise population, and may already be of little value for porpoise conservation. Five high-priority porpoise conservation sites and five sections that now contain few or no surviving porpoises are identified. Proposed spatial modifications to existing reserves and associated conservation recommendations are made for five existing protected areas along the Yangtze main stem, and we emphasize that some additional river sections should urgently be designated as new protected areas given their high porpoise density. Our approach for identifying conservation priorities may provide lessons for reserve design and management in other protected area networks.

Week of 14 January 2013

Allen CD, Lemons GE, Eguchi T, LeRoux RA, Fahy CC, Dutton PH, Peckham SH, Seminoff JA. 2013. Stable isotope analysis reveals migratory origin of loggerhead turtles in the Southern California Bight. *Marine Ecology Progress Series* 472: 275–285.

Abstract - Loggerhead turtles *Caretta caretta* in the North Pacific are listed as Endangered under the US Endangered Species Act and the IUCN Red List. Due partly to their imperiled status, the US National Marine Fisheries Service established a time-area closure in 2003 for the California drift gillnet (CDGN) fishery operating within the Southern California Bight (SCB) to avoid incidental captures. This closure is triggered when sea surface temperatures are above normal, generally caused by El Niño-derived warm-water conditions, which is the time when loggerheads are thought to enter the SCB. Knowledge of the previous foraging grounds of loggerheads incidentally captured by the CDGN fishery in the SCB will help elucidate the oceanographic mechanisms that may influence turtle movement into this region and can assist in optimizing the environmental triggers for implementation of the SCB fishing closure. Stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope analysis was used to determine the previous foraging grounds of loggerheads encountered in the SCB. Skin samples from loggerheads captured in the CDGN fishery were compared with skin from loggerheads in the central North Pacific, incidentally caught in the Hawaii-based longline fishery, as well as skin from turtles sampled during in-water research along the Baja California Peninsula, Mexico. The stable isotope values of CDGN-caught turtles were more similar to those from the central North Pacific than to those from Baja, indicating movements from the central North Pacific to the SCB. We elaborate on potential oceanographic mechanisms by which turtles access the SCB and provide insights that can inform future management decisions for the time-area closure.

Curtis KA, Moore JE. 2013. Calculating reference points for anthropogenic mortality of marine turtles. *Aquatic Conservation: Marine and Freshwater Ecosystems*. DOI:10.1002/aqc.2308
<http://onlinelibrary.wiley.com/doi/10.1002/aqc.2308/abstract>

Abstract - 1. Human-caused mortality threatens many marine turtle populations worldwide, with fisheries interactions being a primary cause for population declines. National and international management of fisheries interactions with marine turtles are rarely tied to turtle population biology. Quantitative tools tied to population-based objectives can provide insight into the effectiveness and urgency of bycatch mitigation. 2. A management approach is proposed based on a bycatch control rule called Reproductive Value Loss Limit (RVLL), generalized from the Potential Biological Removal management model for marine mammal populations. For RVLL, population size is scaled by reproductive value to account for strongly age-structured population dynamics and age-dependent fisheries mortality rates in marine turtle populations. 3. RVLL is an estimate of maximum sustainable mortality for a population, calculated from estimates of maximum population growth rate, total reproductive value in the population, and an uncertainty factor. RVLL estimates correspond to specified management goals and risk tolerances. For demonstration, simultaneous goals of maintaining populations above the maximum net productivity level (analogous to the population size that produces maximum sustainable yield) and preventing a decrease in adults are assumed, both with 95% probability. A management-strategy-evaluation-like process was used to explore parameterization of the RVLL equation for robust performance over a range of plausible life history characteristics and uncertainties in abundance and bycatch mortality estimates for marine turtle populations. 4. The RVLL-based management approach presented here proved robust to several important sources of uncertainty and to violation of several key underlying assumptions, and can be adapted to account for important sources of bias. The architecture presented, including tailored management strategy evaluation, provides a useful basis for further development of reference-point-based management of human-added mortality in populations that experience large changes with age in reproductive value and human-caused mortality rates, as is the case for marine turtles.

Week of 7 January 2013

Staaf, D.J., **J.V. Redfern**, W.F. Gilly, W. Watson, and **L.T. Ballance**. 2013. Distribution of ommastrephid paralarvae in the eastern tropical Pacific. *Fishery Bulletin* 111:78-89.

Abstract—Jumbo squid (*Dosidicus gigas*) and purpleback squid (*Sthenoteuthis oualaniensis*) (Teuthida: Ommastrephidae) are thought to spawn in the eastern tropical Pacific. We used 10 years of plankton tow and oceanographic data collected in this region to examine the reproductive habits of these 2 ecologically important squid. Paralarvae of jumbo squid and purpleback squid were found in 781 of 1438 plankton samples from surface and oblique tows conducted by the Southwest Fisheries Science Center (NOAA) in the eastern tropical Pacific over the 8-year period of 1998–2006. Paralarvae were far more abundant in surface tows (maximum: 1588 individuals) than in oblique tows (maximum: 64 individuals). A generalized linear model analysis revealed sea-surface temperature as the strongest environmental predictor of paralarval presence in both surface and oblique tows; the likelihood of paralarval presence increases with increasing temperature. We used molecular techniques to identify paralarvae from 37 oblique tows to species level and found that the purpleback squid was more abundant than the jumbo squid (81 versus 16 individuals).

Turvey ST, Risly CL, **Moore JE**, Barrett LA, Yujiang H, Xiujiang Z, Kaiya Z, Ding W. 2013. Can local ecological knowledge be used to assess status and extinction drivers in a threatened freshwater cetacean? *Biological Conservation* 157:352-360.

Abstract - Local ecological knowledge constitutes a potentially useful source of information for conservation, but the quality, limitations and biases of this body of knowledge remain largely untested. The Yangtze finless porpoise (*Neophocaena asiaeorientalis asiaeorientalis*) is a highly threatened freshwater cetacean found in one of the world's most densely populated human environments. The dynamics of

porpoise decline remain poorly understood, and local ecological knowledge from fishing communities across its range may represent an important conservation tool for monitoring porpoise population status and quantifying levels of human-caused mortality. We used interview data from an extensive survey of fishing communities across the middle-lower Yangtze drainage to investigate spatial and temporal patterns of porpoise abundance, mortality and population change. Interview data on porpoise relative abundance and decline, especially weekly sighting frequencies, show congruent spatial patterns with data collected from boat-based Yangtze cetacean surveys, demonstrating that informant data can provide accurate quantitative information on these two key parameters of species conservation status. Interview-based collection of local ecological knowledge therefore represents a useful monitoring method for assessing population trends in freshwater cetaceans and other charismatic or distinctive aquatic species, and may be particularly appropriate in regions where resources for regular boat-based surveys are limited. Using local ecological knowledge to identify primary threats to the porpoise population is less straightforward due to probable biases in interview data on porpoise mortality. However, interview data are able to demonstrate that the number of porpoises killed annually in the Yangtze mainstream may have doubled, and that annually mortality rate may have quadrupled, over the past two decades, with mortality due to vessel strikes and other factors having increased more in recent years than by-catch mortality. It seems unlikely that fisheries mortality has been the dominant driver of porpoise decline in the Yangtze mainstream, suggesting that regulating regional fisheries may not be sufficient for porpoise conservation.